

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti
Guegler, Karl J.
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10
(B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met	Val	His	Val	Ala	Tyr	Ser	Leu	Cys	Leu	Pro	Met	Arg	Arg	Ser	
				5					10					15	
Glu	Arg	Tyr	Leu	Phe	Leu	Asn	Met	Ala	Tyr	Gln	Gln	Val	His	Ala	
				20					25					30	
Asn	Ile	Glu	Asn	Ser	Trp	Asn	Glu	Glu	Glu	Val	Trp	Arg	Ile	Glu	
				35					40					45	
Met	Tyr	Ile	Ser	Phe	Gly	Ile	Met	Ser	Leu	Gly	Leu	Leu	Ser	Leu	
				50					55					60	
Leu	Ala	Val	Thr	Ser	Ile	Pro	Ser	Val	Ser	Asn	Ala	Leu	Asn	Trp	
				65					70					75	
Arg	Glu	Phe	Ser	Phe	Ile	Gln	Ser	Thr	Leu	Gly	Tyr	Val	Ala	Leu	
				80					85					90	
Leu	Ile	Ser	Thr	Phe	His	Val	Leu	Ile	Tyr	Gly	Trp	Lys	Arg	Ala	
				95					100					105	
Phe	Glu	Glu	Glu	Tyr	Tyr	Arg	Phe	Tyr	Thr	Pro	Pro	Asn	Phe	Val	
				110					115					120	
Leu	Ala	Leu	Val	Leu	Pro	Ser	Ile	Val	Ile	Leu	Asp	Leu	Leu	Gln	
				125					130					135	
Leu	Cys	Arg	Tyr	Pro	Asp										
				140											

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met	Phe	Leu	Pro	Pro	Val	Val	Leu	Ala	Ile	Arg	Ser	Arg	Tyr	Val	
				5					10					15	
Leu	Glu	Ala	Ala	Val	Tyr	Thr	Phe	Thr	Met	Phe	Phe	Ser	Thr	Phe	
				20					25					30	
Tyr	His	Ala	Cys	Asp	Gln	Pro	Gly	Ile	Val	Val	Phe	Cys	Ile	Met	
				35					40					45	
Asp	Tyr	Asp	Val	Leu	Gln	Phe	Cys	Asp	Phe	Leu	Gly	Ser	Leu	Met	
				50					55					60	
Ser	Val	Trp	Val	Thr	Val	Ile	Ala	Met	Ala	Arg	Leu	Gln	Pro	Val	
				65					70					75	
Val	Lys	Gln	Val	Leu	Tyr	Leu	Leu	Gly	Ala	Met	Leu	Leu	Ser	Met	
				80					85					90	
Ala	Leu	Gln	Leu	Asp	Arg	His	Gly	Leu	Trp	Asn	Leu	Leu	Gly	Pro	
				95					100					105	
Ser	Leu	Phe	Ala	Leu	Gly	Ile	Leu	Ala	Thr	Ala	Trp	Thr	Val	Arg	
				110					115					120	
Ser	Val	Arg	Arg	Arg	His	Cys	Tyr	Pro	Pro	Thr	Trp	Arg	Arg	Trp	
				125					130					135	
Leu	Phe	Tyr	Leu	Cys	Pro	Gly	Ser	Leu	Ile	Ala	Gly	Ser	Ala	Val	
				140					145					150	
Leu	Leu	Tyr	Ala	Phe	Val	Glu	Thr	Arg	Asp	Asn	Tyr	Phe	Tyr	Ile	

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His Ser Ile Trp	155	His Met Leu Ile Ala	160	Gly Ser Val Gly Phe Leu	165
Leu Pro Pro Arg	170	Ala Lys Thr Asp His	175	Gly Val Pro Ser Gly Ala	180
Arg Ala Arg Gly	185	Cys Gly Tyr Gln Leu	190	Cys Ile Asn Glu Gln Glu	195
Glu Pro Gly Pro	200	Arg Gly Pro Arg Arg	205	Gly His Cys Gln Gln His	210
Leu Cys Gln Leu	215	Arg Gly Ala Leu Gly	220	Leu Ala Leu Arg Gly Tyr	225
Glu Cys Phe Leu	230	Glu Phe Phe Leu Gly	235	Val Trp Ser Pro Leu Arg	240
Arg Arg Gln Ala	245	Val Phe Leu Glu Asp	250	Met Glu Ser Phe Ser Arg	255
Thr Gln Asn Ser	260	Ser Arg Asp Leu Glu	265	Pro Phe Pro Gly His Gly	270
Glu Leu Pro Glu	275	Gly Leu Glu Ser Pro	280	Cys Ile Met Glu Ser Phe	285
Leu Arg Thr Gly	290	Ala Tyr Ala Gly Thr	295	Glu Ser Leu Arg Thr Lys	300
Glu Ser Leu Leu	305	Gln Val Trp Ser Leu	310	Ser Trp Asp Ala Glu Pro	315
Ser Gln Asp Met	320	Asp Ser Phe Pro Gly	325	Arg Gln Ser Pro Val Arg	330
Ser Thr Ala Ser	335	Phe Gln Arg Arg Trp	340	Ser Leu Ser Trp Gly Asn	345
Gln Ile Ser Arg	350	Phe Ser Gln Arg Leu	355	Ser Asn Ser Gly Leu Arg	360
Leu Pro Ser Gln	365	Arg Gln Arg Leu Gly	370	Cys Ala Val Leu Trp Arg	375
Arg Asp Cys Arg	380	Met Asp Gly Ala Gly	385	Thr Gly Ala Val Trp Val	390
Ala Gly Ile Leu	395	Val	400		405
	410				

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAGG	AGATTTCCAC	CTTGGTTGGA	AACCTGGTTA	CAGTGTAGAA	AACAGCTTGG	60
ATTACTAAGT	TTTTTCTTCG	CTATGGTCCA	TGTTGCCCTAC	AGCCTCTGCT	TACCGATGAG	120
AAGGTCAGAG	AGATATTTGT	TTCTCAACAT	GGCTTATCAG	CAGGTTTCATG	CAAATATTGA	180
AAACTCTTGG	AATGAGGAAG	AAGTTTGGAG	AATTGAAATG	TATATCTCCT	TTGGCATAAT	240
GAGCCTTGGC	TTACTTTCCC	TCCTGGCAGT	CACCTCTATC	CCTTCAGTGA	GCAATGCTTT	300
AAACTGGAGA	GAATTCAGTT	TTATTCAGTC	TACACTTGGA	TATGTCGCTC	TGCTCATAAG	360
TACTTTCCAT	GTTTTAATTT	ATGGATGGAA	ACGAGCTTTT	GAGGAAGAGT	ACTACAGATT	420
TTATACACCA	CCAAACTTTG	TTCTTGCTCT	TGTTTTGCCC	TCAATTGTAA	TTCTGGATCT	480

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TTTGCAGCTT	TGCAGATACC	CAGACTGAGC	TGGAAGTGGG	ATTTGTCTTC	CTATTGACTC	540
TACTTCTTTA	AAAGCGGCTG	CCCATTACAT	TCCTCAGCTG	TCCTTGCACT	TAGGTGTACA	600
TGTGACTGAG	TGTTGGCCAG	TGAGATGAAG	TCTCCTCAAA	GGAAGGCAGC	ATGTGTCCTT	660
TTTCATCCCT	TCATCTTGCT	GCTGGGATTG	TGGATATAAC	AGGAGCCCTG	GCAGCTGTCT	720
CCAGAGGATC	AAAGCCACAC	CCAAAGAGTA	AGGCAGATTA	GAGACCAGAA	AGACCTTGAC	780
TACTTCCCTA	CTTCCACTGC	TTTTTCCTGC	ATTTAAGCCA	TTGTAAATCT	GGGTGTGTTA	840
CATGAAGTGA	AAATTAATTC	TTTCTGCCCT	TCAGTTCTTT	ATCCTGATAC	CATTTAACAC	900
TGTCTGAATT	AACTAGACTG	CAATAATTCT	TTCTTTTGAA	AGCTTTTAAA	GGATAATGTG	960
CAATTCACAT	TAAAATTGAT	TTTCCATTGT	CAATTAGTTA	TACTCATTTT	CCTGCCTTGA	1020
TCTTTTATTA	GATATTTTGT	ATCTGCTTGG	AATATATTAT	CTTCTTTTTT	ACTGTGTAAT	1080
TGGTAATTAC	TAAAACCTCT	TAATCTCCAA	AATATTGCTA	TCAAATTACA	CACCATGTTT	1140
TCTATCATTC	TCATAGATCT	GCCTTATAAA	CATTTAAATA	AAAAGTACTA	TTTAATGATT	1200
TAAAAAATAA	AAA					1213

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG	GGCTGCTCTG	CCTGAGCAAC	CTCATGTTTC	TGCCACCTGT	GGTCCCTGGCC	60
ATTCGGAGTC	GATATGTGCT	GGAAGCTGCA	GTCTACACCT	TCACCATGTT	CTTCTCCACG	120
TTCTATCATG	CCTGTGACCA	GCCAGGCATC	GTGGTTTTCT	GCATCATGGA	CTACGATGTG	180
CTGCAGTTCT	GTGATTTTCT	GGGCTCCCTA	ATGTCCGTGT	GGGTCACTGT	CATTGCCATG	240
GCTCGTTTTAC	AGCCCGTGGT	CAAGCAGGTG	CTGTATTTGC	TGGGAGCTAT	GCTGCTGTCC	300
ATGGCTCTGC	AGCTTGACCG	ACATGGACTC	TGGAACCTGC	TTGGACCCAG	TCTCTTCGCC	360
CTGGGGATCT	TGGCCACAGC	CTGGACAGTA	CGCAGCGTCC	GCCGCCGGCA	CTGTACCCA	420
CCCACGTGGC	GCCGCTGGCT	TTTCTACTTG	TGCCCTGGCA	GCCTTATTGC	AGGCAGTGCC	480
GTCCTGCTTT	ATGCTTTTGT	GGAGACCCGG	GACAACACT	TCTACATTCA	CAGCATTTGG	540
CATATGCTCA	TTGCGGGCAG	TGTGGGCTTC	CTGCTGCCCC	CTCGTGCCAA	GACTGACCAC	600
GGGGTCCCAT	CTGGAGCCCG	GGCCCCGGGG	TGTGGTTACC	AGCTATGCAT	CAACGAGCAG	660
GAGGAGCCTG	GGCCTCGTGG	GCCCAGGAGG	GGCCACTGTC	AGCAGCATCT	GTGCCAGCTG	720
AGAGGGGCTT	TGGGCCTGGC	CCTGAGGGGA	TATGAATGCT	TCCTAGAGTT	CTTTCTGGGG	780
GTGTGGAGCC	CTCTTAGAAG	GAGACAGGCT	GTATTTCTTG	AGGACATGGA	GTCTTTCTCA	840
AGGACACAAA	ACTCTTCCAG	GGACCTGGAG	CCCTTCCCAG	GACATGGAGA	ACTTCCTGAG	900
GGCCTGGAGT	CCCCCTGCAT	CATGGAGTCC	TTCTTAAGGA	CTGGAGCCTA	TGCAGGCACA	960
GAGTCCCTCA	GGACCAAGGA	GTCCCTCCTG	CAGGTGTGGA	GCCTTTCCTG	GGATGCAGAG	1020
CCTTCCCAAG	ACATGGATTG	CTTCCCAGGG	AGACAAAGCC	CTGTCAGGAG	CACAGCATCT	1080
TTCCAGAGGA	GGTGGAGTCT	ATCTTGGGGA	AACCAATTT	CCAGATTTTC	CCAGAGGCTC	1140
AGCAACTCTG	GCCTCAGGCT	TCCTTCCCAG	AGGCAGCGTC	TGGGCTGTGC	TGTGCTGTGG	1200
AGGAGGGATT	GCAGGATGGA	TGGAGCTGGG	ACTGGGGCTG	TCTGGGTGGC	TGGTATCCTC	1260
GTTTGATACA	GGTGGAGTCT	CTGTGTCTCC	ATAGAAG			1297

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met	Gly	Arg	Ala	Met	Val	Val	Arg	Leu	Gly	Leu	Gly	Leu	Leu	Leu	
				5					10					15	
Leu	Ala	Leu	Leu	Leu	Pro	Thr	Gln	Ile	Tyr	Cys	Asn	Gln	Thr	Ser	
				20					25					30	
Val	Ala	Pro	Phe	Ser	Gly	Asn	Gln	Ser	Ile	Ser	Ala	Ala	Pro	Asn	
				35					40					45	
Pro	Thr	Asn	Ala	Thr	Thr	Arg	Ser	Gly	Cys	Ser	Ser	Leu	Gln	Ser	
				50					55					60	
Thr	Ala	Gly	Leu	Leu	Ala	Leu	Ser	Leu	Ser	Leu	Leu	His	Leu	Tyr	
				65					70					75	
Cys															

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met	Trp	Val	Pro	Val	Val	Phe	Leu	Thr	Leu	Ser	Val	Thr	Trp	Ile	
				5					10					15	
Gly	Ala	Ala	Pro	Leu	Ile	Leu	Ser	Arg	Ile	Val	Gly	Gly	Trp	Glu	
				20					25					30	
Cys	Glu	Lys	His	Ser	Gln	Pro	Trp	Gln	Val	Leu	Val	Ala	Ser	Arg	
				35					40					45	
Gly	Arg	Ala	Val	Cys	Gly	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	
				50					55					60	
Leu	Thr	Ala	Ala	His	Cys	Ile	Arg	Asn	Lys	Ser	Val	Ile	Leu	Leu	
				65					70					75	
Gly	Arg	His	Ser	Leu	Phe	His	Pro	Glu	Asp	Thr	Gly	Gln	Val	Phe	
				80					85					90	
Gln	Val	Ser	His	Ser	Phe	Pro	His	Pro	Leu	Tyr	Asp	Met	Ser	Leu	
				95					100					105	
Leu	Lys	Asn	Arg	Phe	Leu	Arg	Pro	Gly	Asp	Asp	Ser	Ser	His	Asp	
				110					115					120	
Leu	Met	Leu	Leu	Arg	Leu	Ser	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Ala	
				125					130					135	
Val	Lys	Val	Met	Asp	Leu	Pro	Thr	Gln	Glu	Pro	Ala	Leu	Gly	Thr	
				140					145					150	
Thr	Cys	Tyr	Ala	Ser	Gly	Trp	Gly	Ser	Ile	Glu	Pro	Glu	Glu	Phe	
				155					160					165	
Leu	Thr	Pro	Lys	Lys	Leu	Gln	Cys	Val	Asp	Leu	His	Val	Ile	Ser	
				170					175					180	
Asn	Asp	Val	Cys	Ala	Gln	Val	His	Pro	Gln	Lys	Val	Thr	Lys	Phe	
				185					190					195	

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Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser
				200					205					210
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly
				215					220					225
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro
				230					235					240
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp
				245					250					255
Thr	Ile	Val	Ala	Asn	Pro									
				260										

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys
				5					10					15
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser
				20					25					30
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val
				35					40					45
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln
				50					55					60
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg
				65					70					75
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly
				80					85					90
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln
				95					100					105
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln
				110					115					120
Met	Gln	Phe	Leu	Glu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His
				125					130					135
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro
				140					145					150
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly
				155					160					165
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro
				170					175					180
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu
				185					190					195
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg
				200					205					210
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr
				215					220					225
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala
				230					235					240
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val

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Asp Glu Val His	245	Val Asp Gln Thr Lys Ser	255
Ser Asn Val Trp	260	Ile Trp Glu Leu Phe Glu	270
Leu Gly Ala Gln	275	Ser Asp Arg Gln Val Leu	285
Ala Tyr Ala Val	290	Lys Leu Pro Lys Pro Gln	300
Leu Gln Leu Ala	305	Tyr Glu Val Met Gln Phe	315
Cys Trp Leu Gln	320	Thr Ala Glu Glu Val His	330
Leu Leu Leu Ser	335	Gly Thr Thr Glu Leu Glu	345
Glu Glu Phe Glu	350	Leu Arg Pro Gly Gly Ser	360
Thr Gly Leu Gly	365	Pro Ala Ala Ala Thr Ala	375
Ala Ser Ala Glu	380	Ser Phe Pro Leu Leu Glu	390
Arg Phe Thr Ser	395	Asp Ser Asp Asp Val Leu	405
Thr Val Thr Glu	410	Asn Phe Glu Tyr Lys Trp	420
Glu Ala Gly Cys	425	Pro Pro Ser Gly Ala Ala	435
Ser Ser Pro Gly	440	Gln Glu Leu Cys Ala Pro	450
Asp Ser Ser Pro	455	Val Leu Ser Ala His Ser	465
Pro Ser Val Gly	470	Arg Leu Glu Gly Ala Val	480
Pro Ala Ala Gly	485	Ala Gly Cys Ala Pro Ser	495
Pro Gln Ala Val	500	Asn Ser Glu Glu Ser Thr	510
Val Ala Ser Leu	515	Leu Gly His Ala Pro Pro	525
Thr Glu Gly Leu	530	His His Ser His Arg Arg	540
Gln Gly Ser Pro	545	Pro Ser Pro Gly Thr Pro	555
Met Leu Pro Ala	560	Gly Val Ala Thr Phe Cys	570
Pro Pro Phe Phe	575	Ala Ser Pro Ser Gly Ser	585
Pro Gly Ala Gln	590	Glu Glu Pro Glu Glu Gly	600
Lys Val Gly Leu	605	His Trp Ser Ser Asn Met	615
Ser Ala Asn Asn	620	Asp Pro Glu Ser Trp Asp	630
Pro Gly Tyr Val	635	Ser Tyr Arg Asp Asp Cys	645
Ser Ser Leu Glu	650	Ser Pro Glu Val Gly His	660
Leu Leu Ser Gln	665	Phe Leu Pro Gly Leu Val	675
Ala Val Ser Pro	680	Arg Pro Phe Asn Leu Leu	690
	695		705

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Pro	Leu	Cys	Pro	Ala	Lys	Gly	Leu	Ala	Pro	Ala	Ala	Cys	Leu	Ile			
				710					715					720			
Thr	Ser	Pro	Trp	Thr	Glu	Gly	Ala	Val	Gly	Gly	Ala	Glu	Asn	Pro			
				725					730					735			
Ile	Val	Glu	Pro	Lys	Leu	Ala	Gln	Glu	Ala	Glu	Gly	Ser	Ala	Glu			
				740					745					750			
Pro	Gln	Leu	Pro	Leu	Pro	Ser	Val	Pro	Ser	Pro	Ser	Cys	Glu	Gly			
				755					760					765			
Ala	Ser	Leu	Pro	Ser	Glu	Glu	Ala	Ser	Ala	Pro	Asp	Ile	Leu	Pro			
				770					775					780			
Ala	Ser	Pro	Thr	Pro	Ala	Ala	Gly	Ser	Trp	Val	Thr	Val	Pro	Glu			
				785					790					795			
Pro	Ala	Pro	Thr	Leu	Glu	Ser	Ser	Gly	Ser	Ser	Leu	Gly	Gln	Glu			
				800					805					810			
Ala	Pro	Ser	Ser	Glu	Asp	Glu	Asp	Thr	Thr	Glu	Ala	Thr	Ser	Gly			
				815					820					825			
Val	Phe	Thr	Asp	Leu	Ser	Ser	Asp	Gly	Pro	His	Thr	Glu	Lys	Ser			
				830					835					840			
Gly	Ile	Val	Pro	Ala	Leu	Arg	Ser	Leu	Gln	Lys	Gln	Val	Gly	Thr			
				845					850					855			
Pro	Asp	Ser	Leu	Asp	Ser	Leu	Asp	Ile	Pro	Ser	Ser	Ala	Ser	Asp			
				860					865					870			
Gly	Gly	Cys	Glu	Val	Leu	Ser	Pro	Ser	Ala	Ala	Gly	Pro	Pro	Gly			
				875					880					885			
Gly	Gln	Pro	Arg	Ala	Val	Asp	Ser	Gly	Tyr	Asp	Thr	Glu	Asn	Tyr			
				890					895					900			
Glu	Ser	Pro	Glu	Phe	Val	Leu	Lys	Glu	Ala	His	Glu	Ser	Ser	Glu			
				905					910					915			
Pro	Glu	Ala	Phe	Gly	Glu	Pro	Ala	Ser	Glu	Gly	Glu	Ser	Pro	Gly			
				920					925					930			
Pro	Asp	Pro	Leu	Leu	Ser	Val	Ser	Leu	Gly	Gly	Leu	Ser	Lys	Lys			
				935					940					945			
Ser	Pro	Tyr	Arg	Asp	Ser	Ala	Tyr	Phe	Ser	Asp	Leu	Asp	Ala	Glu			
				950					955					960			
Ser	Glu	Pro	Thr	Phe	Gly	Pro	Glu	Lys	His	Ser	Gly	Ile	Gln	Asp			
				965					970					975			
Ser	Gln	Lys	Glu	Gln	Asp	Leu	Arg	Ser	Pro	Pro	Ser	Pro	Gly	His			
				980					985					990			
Gln	Ser	Val	Gln	Ala	Phe	Pro	Arg	Ser	Ala	Val	Ser	Ser	Glu	Val			
				995					1000					1005			
Leu	Ser	Pro	Pro	Gln	Gln	Ser	Glu	Glu	Pro	Leu	Pro	Glu	Val	Pro			
				1010					1015					1020			
Arg	Pro	Glu	Pro	Leu	Gly	Ala	Gln	Gly	Pro	Val	Gly	Val	Gln	Pro			
				1025					1030					1035			
Val	Pro	Gly	Pro	Ser	His	Ser	Lys	Cys	Phe	Pro	Leu	Thr	Ser	Val			
				1040					1045					1050			
Pro	Leu	Ile	Ser	Glu	Gly	Ser	Gly	Thr	Glu	Pro	Gln	Gly	Pro	Ser			
				1055					1060					1065			
Gly	Gln	Leu	Ser	Gly	Arg	Ala	Gln	Gln	Gly	Gln	Met	Gly	Asn	Pro			
				1070					1075					1080			
Ser	Thr	Pro	Arg	Ser	Pro	Leu	Cys	Leu	Ala	Leu	Pro	Gly	His	Pro			
				1085					1090					1095			
Gly	Ala	Leu	Glu	Gly	Arg	Pro	Glu	Glu	Asp	Glu	Asp	Thr	Glu	Asp			
				1100					1105					1110			
Ser	Glu	Glu	Ser	Asp	Glu	Glu	Leu	Arg	Cys	Tyr	Ser	Val	Gln	Glu			
				1115					1120					1125			
Pro	Ser	Glu	Asp	Ser	Glu	Glu	Glu	Pro	Pro	Ala	Val	Pro	Val	Val			
				1130					1135					1140			
Val	Ala	Glu	Ser	Gln	Ser	Ala	Arg	Asn	Leu	Arg	Ser	Leu	Leu	Lys			
				1145					1150					1155			
Met	Pro	Ser	Leu	Leu	Ser	Glu	Ala	Phe	Cys	Asp	Asp	Leu	Glu	Arg			

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	1160		1165		1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr Leu					
	1175		1180		1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly Glu Pro Phe Pro					
	1190		1195		1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu Gly Gly Pro Ser					
	1205		1210		1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala Gly His Ser Pro					
	1220		1225		1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg Phe Glu Trp Asp Gly					
	1235		1240		1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala Leu Val Thr Glu Leu					
	1250		1255		1260
Asp Pro Ala Asp Pro Val Leu Ala Ala Pro Pro Thr Pro Ala Ala					
	1265		1270		1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro Ala Ser Arg Phe					
	1280		1285		1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln Ser Val Gly Gly					
	1295		1300		1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala					
	1310		1315		

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